

GGCCAGTGGGGGTGGCTGCGGCTGCTACATGCCCCACGGACCAGAACCTCCCGACGCGGCCAGGCCCCGGC ACACCCAGCTGCAGAAAGGAGAGAAAATCCCTTGGCTCTAAAATGACATCTGGAGAAGTGAAGACAAGCCTCAAGAA TGCCTACTCATCTGCCAAGAGGCTGTCGCCGAAGATGGAGGAGGAGGAGGAGGAGGAGGACTACTGCACCCCTGGAG CCTTTGAGCTGGAGCGGCTCTTCTGGAAGGGCAGTCCCCAGTACACCCACGTCAACGAGGTCTGGCCCAAGCTCTAC $\tt CGGCCGCTGGAACGTGGACACTGGGCCCGACTACTACCGCGACATGGACATCCAGTACCACGGCGTGGAGGCCGACG$ ACCTGCCCACCTTCGACCTCAGTGTCTTCTTCTACCCGGCGGCAGCCTTCATCGACAGAGCGCTAAGCGACGACCAC AGTAAGATCCTGGTTCACTGCGTCATGGGCCGCAGCCGGTCAGCCACCCTGGTCCTGGCCTACCTGATGATCCACAA GGACATGACCCTGGTGGACGCCATCCAGCAAGTGGCCAAGAACCGCTGCGTCCTCCCGAACCGGGGCTTTTTGAAGC AGCTCCGGGAGCTGGACAAGCAGCTGGTGCAGCAGAGGCGACGGTCCCAGCGCCCAGGACGGTGAGGAGGAGGATGGC CTAGGACTCCAGAGAAGGGATGGTGAAACCGAAGCTCGACTCTTCCAAACCATCTTGTTCAACTTCCCCATGTGTGC AAAAAAAAA

FIGURE 1

Translation- 220 amino acids

MTSGEVKTSLKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQ KAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRS ATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQRRRSQRQDGEEEDGREL

FIGURE 2

20 60		130 140 150 160 170 180183	FPERISFIDEA-RGKNCGVLYHCLAGISRSYTYTYAYLMQKLNLSMNDAYDIVKMKSNISPNFNFMGQLLDFERTLGLSS FPERISFIDEA-RSKKCGVLYHCLAGISRSYTYTYAYLMQKLNLSNNDAYDIVKMKSNISPNFNFMGQLLDFERTLGLSS FPERISFIDEA-LSQNCGVLYHCLAGISRSYTYTYAYLMQKHNLSLNDAYDLVKRKKSNISPNFNFMGQLLDFERSLRLE LDKSIEFIDKA-KLSGCQVIVHCLAGISRSATIAIAYIHKTHGMSSDDAYRFVKDRRPSISPNFNFLGQLLQLEYERTLKLLA FQERISFIDSY-KNSGGRVLYHCQAGISRSATICLAYLMRTNRVKLDEAFDFVKQRRGVISPNFSFMGQLLQLETQVLCH FMERIEYIDBY-KDCRGRVLYHCQAGISRSATICLAYLMMKRVYKLDEAFEVKQRRSIISPNFSFMGQLLQFESQVLATS FMERIEYIDAY-KDCRGRVLYHCQAGISRSATICLAYLMMKRVYKLEEAFEVKQRRSIISPNFSFMGQLLQFESQVLATS FQERIDFIDCY-REKGGKVLYHCCAGISRSPTICHAYLMMKRVRLEEAFEFVKQRRSIISPNFSFMGQLLQFESQVLATS FERRADFIDGALAQKNGRSKSATLVHCYHGRSRSATLVLAYLMHRQKMDVKSALSIVRQNRR-IGPNDGFLRQLRQCLNDRLAKEG
0 20	SOLDRO-PNSATDSDGSPLSNSQPSF DRELPSSATESDGSPVPSSQPAF GATPPPVGLRASF GLCEGKPARLLPHSLSQPCLPVPSVG PRQALPPGGENSNSDPRVPIYDQGG PLSTSVPDSAESGCSSCSTPLYDQGG SERALISQCGKPVVNVSYRPAYDQGG SGSFELSVQDLNDLLSDGSGCYSLPSQP EGEEEDYCTPGAFELERLFWKGSPQYTH	01 110 120	FPERISFIDER-RGKNCGVLVHCLRGIS FPERISFIDER-RSKKGGVLVHCLRGIS FPERIEFIDER-LSGNCGVLVHCLRGIS LDKSIEFIDKR-KLSGCQVIVHCQRGIS FQERISFIDSY-KNSGGRVLVHCQRGIS FNERIEFIDRY-KDCRGRVLVHCQRGIS FRERRDFIDGRLSGNCKVLVHCCRGIS FFRRRDFIDGRLSDHSKILVHCVHGRS
1 10	SDLDRD-I DRELL GLCEGKPI PRQRLPPI PLSTSVPI PVPPSATI SERRLISI SGSFELSVQI EGEEEDYCTI	101 110	FPERISFIDI FPERISFIDI FPERIEFIDI LOKSIEFIDI FQERISFIDI FNERIDFIDI FQERIDFIDI FERRHOFIDI FYPRARFIDI
	PYST1 MKP-7 MKP-4, hVH5 PRC1 MKP-2, MKP-5, MKP-5 VHR DSP-14 Consensus		PYST1 MKP-7 MKP-4, hVH5 PRC1 MKP-2, MKP-2, MKP-5